

YY-1 AP-1

SAA1 --TAGATATG AACTCAGAGG GACTTCATTT CAGAGGCATC TGCCATGTGG<sup>-391</sup>

SAA2 TTTAGACATG AACTCACAGG GATTTTCAGT- CAGGGTCATC TGCCATGTGG<sup>-397</sup>

\*\*\*\*\*

AP-2 NFIL-6/YY-1

SAA1 CCCAGCAGAG CCCATCCTGA GGAAATGACT GGTAGAGTCA GGAGCTGGCT<sup>-341</sup>

SAA2 CCCAGCAGGG CCCATCCTGA GGAAATGACC GGTATAGTCA GGAGCTGGCT<sup>-347</sup>

\*\*\*\*\*

YY-1

SAA1 TCAAAGCTGC CCTCACTTCA CACCTTCCAG CAGCCCAGGT GCCGCCATCA<sup>-291</sup>

SAA2 GAAGAGCTGC CCTCACTCCA CACCTTCCAG CAGCCCAGGT GCCGCCATCA<sup>-297</sup>

\* \*\*\*\*\*

NFkB AP-2 SAF

SAA1 CGGGGCTCCC ACTCTCAACT CCGCAGCCTC AGCCCCCTCA ATGCTGAGGA<sup>-241</sup>

SAA2 CGGGGCTCCC ACTGGCATCT CTGCAGCTGC ACTTCCCCCA ATGCTGAGGA<sup>-247</sup>

\*\*\*\*\*

-240

SAA1 GCAGAGCTGG TCTCCTGCCC TGACAGCTGC CA-GGCACA- -----TC<sup>-201</sup>

SAA2 GCAGAGCTGA TCTAGACCCC TGTCCATTGC CAAGGCACAG CAAACCTCTC<sup>-197</sup>

\*\*\*\*\*

-200 GRE NF-IL6/STAT AP-1.....

SAA1 TTGTTCCCTC AGGTTGCACA ACTGGGATAA ATGACCCGGG ATGAAGAAAC<sup>-151</sup>

SAA2 TTGTTCCCAT AGGTTACACA ACTGGGATAA ATGACCCGGG ATGAAGAAAC<sup>-147</sup>

\*\*\*\*\*

-150 YY-1

SAA1 CACTGGCATC CAGGAAGTTG TCTTAGACCG TTTTGTAGGG GAAATGACCT<sup>-101</sup>

SAA2 CACCGGCATC CAGGAAGTTG TCTTAGACCA GTTTGTAGGG GAAATGACCT<sup>-97</sup>

\*\*\*\*\*

-100 NFkB

SAA1 GCAGGGACTT TCCCAGGGA CCACATCCAG CTTTTCTTCC CTCCAAGAA<sup>-51</sup>

SAA2 GCAGGGACTT TCCCAGGGA CCACATCCAG CTTTTCTTCC CTCCAAGAG<sup>-47</sup>

\*\*\*\*\*

-50 SP-1

SAA1 ACCAGCAGGG AAGGCTCAGT ATAAATAGCA GCCACCGCTC CCTGGCAGGC<sup>-1</sup>

SAA2 ACCAGCA--- -AGGCTCACT ATAAATAGCA GCCACCTCTC CCTGGCAGAC<sup>-1</sup>

\*\*\*\*\*

FIG. 1

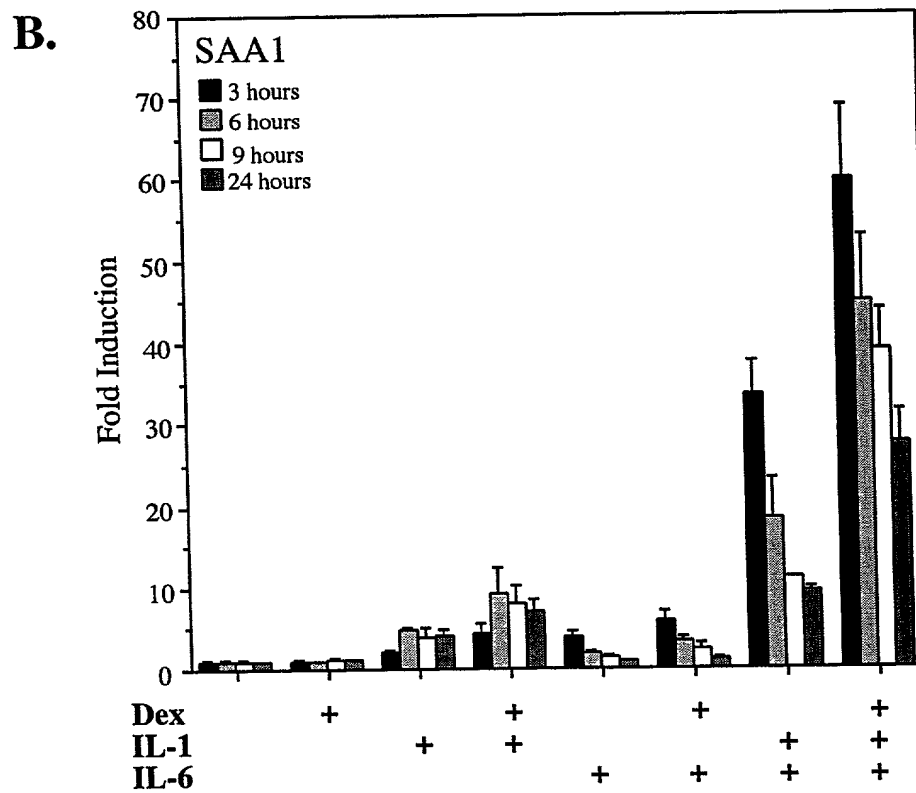
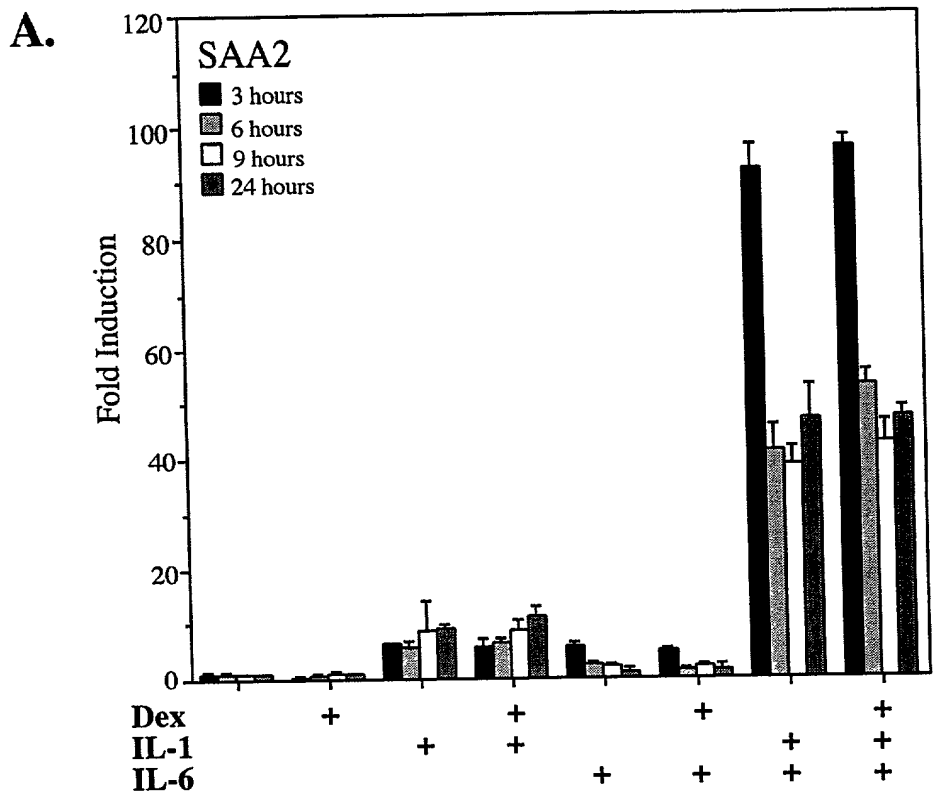


FIG. 2

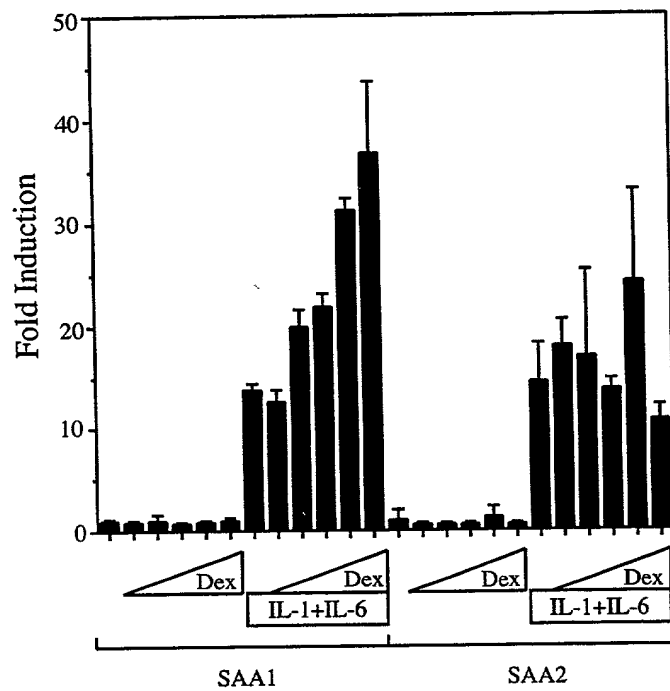


FIG. 3

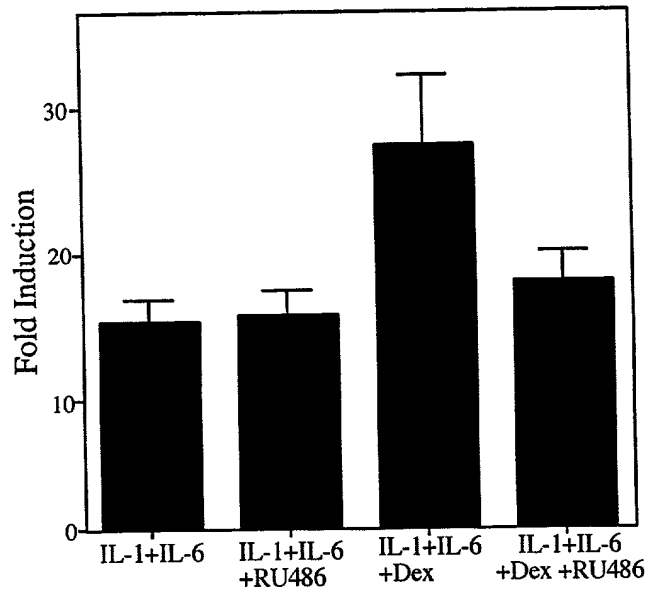


FIG. 4

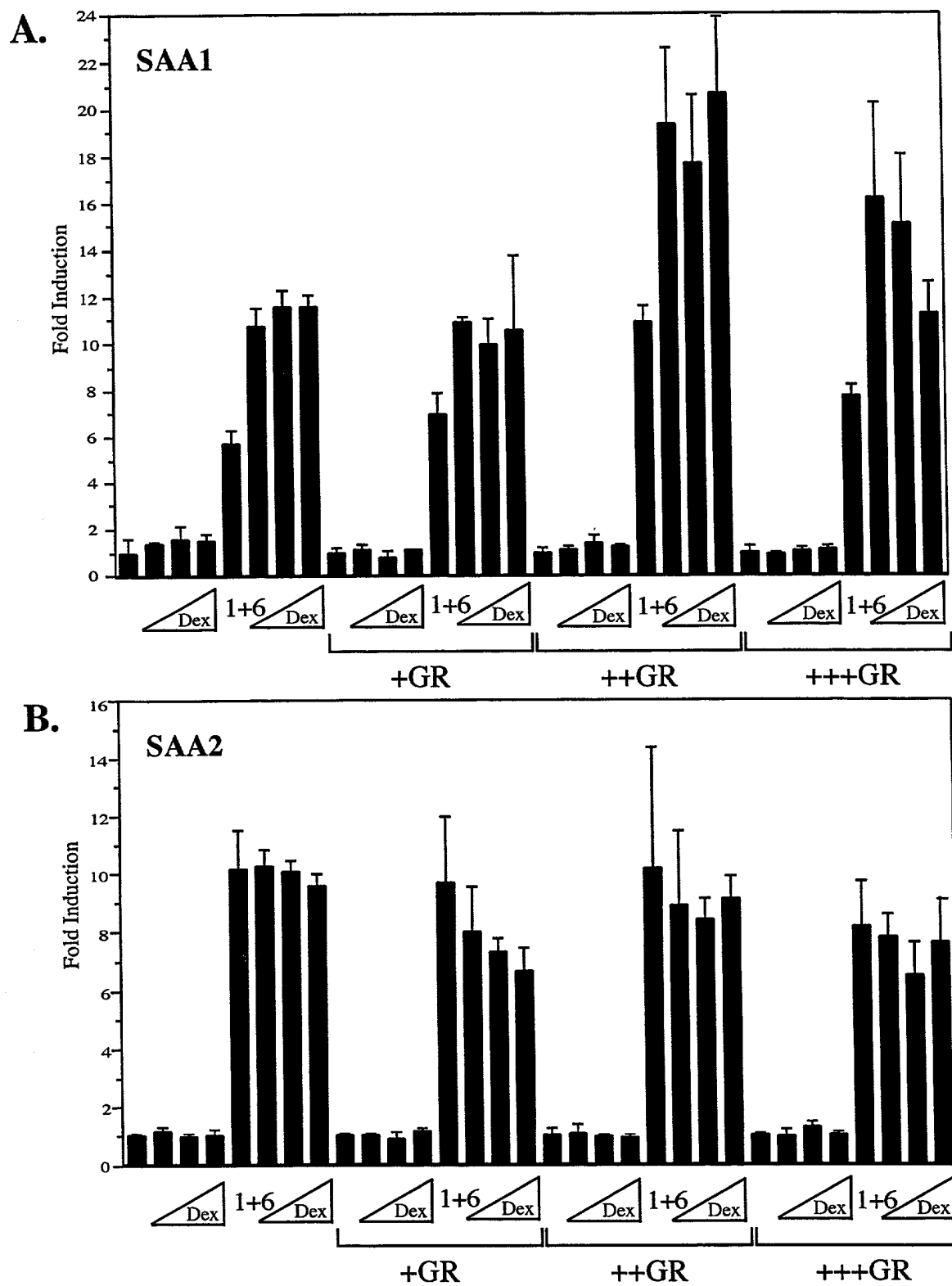


FIG. 5



A.

SAA1	CA- <u>GGCACA</u> -----TCTTGTTCCCTCAGGTTGCACA
GREI	CA-GGCACAGCAAACCTCTCTTGTTCCCTCAGGTTGCACA
GRED	CAAGGCACA-----TCTTGTTCCCATAGGTTACACA
SAA2	CAAGGCACAGCAAACCTCTCTTGTTCCCATAGGTTACACA
Consensus	GGTACA NNNTGTTCT
GRE	

B.

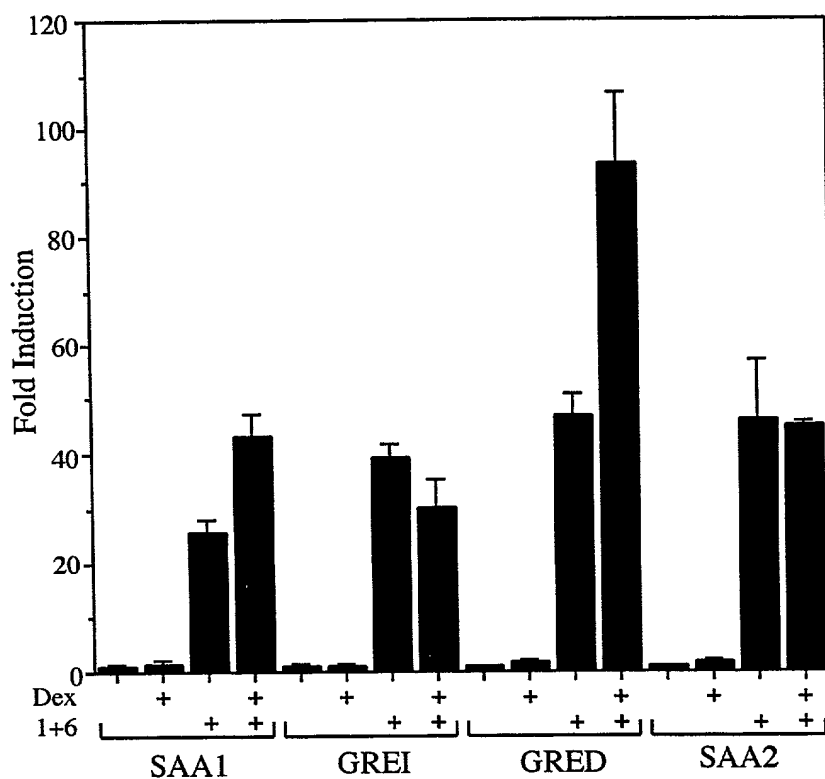


FIG. 7

## A.

SAA1 CAGACAAATACTTCCATGCTCGGGGGAACTATGATGCTGCCAAAAGGGGACCTGGGGGTG<sup>246</sup>  
SAA2 CAGACAAATACTTCCATGCTCGGGGGAACTATGATGCTGCCAAAAGGGGACCTGGGGGTG<sup>246</sup>

                    exon3    exon4

SAA1 TCTGGGCTGCAGAAGCGATCAG|CGATG—//—//—TGAGCTTCCTCTTCACTCTGCTC<sup>426</sup>  
SAA2 CCTGGGCCGCAGAAGTGATCAG|CAATG—//—//—TGAGCTTCCTCTTCACTCTGCTC<sup>426</sup>

SAA1 TCAGGAGATCTGGCTGTGAGGC-TCAGGGCAGGGATACAAAGC-----GGGG-----<sup>472</sup>  
SAA2 TCAGGAGACCTGGCTATGAGCCCTCGGGGCAGGGATTCAAAGTTAGTGAGGTCTATGTCC<sup>486</sup>

SAA1 AGAG-----GGTACACAATGGGTATCTAATAAATACTTAAGAGGTGGAAAAAA<sup>520</sup>  
SAA2 AGAGAAGCTGAGATATGGCATATAATAGGCATCTAATAAATGCTTAAGAGGTGGAAAAAA<sup>546</sup>

## B.

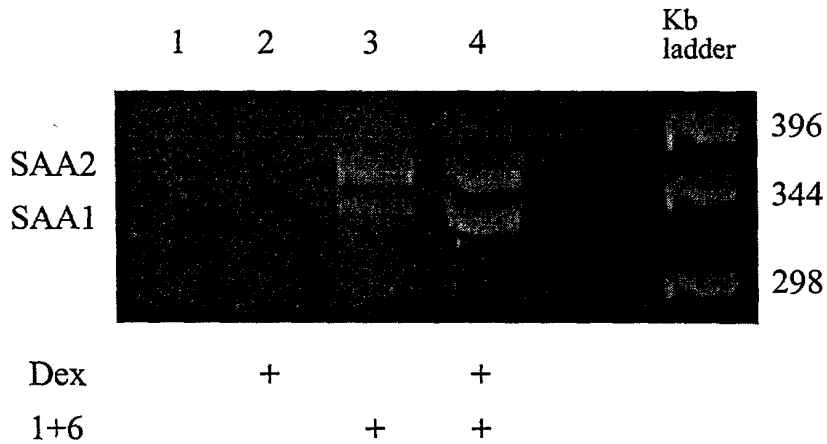


FIG. 8